

CRF Errors Corrected by the STIC Systems Branch

CRF Processing Date:

Edited by:

Verified by:

(STIC staff)

Serial Number: 09/771,904A

1600#21
2/24/2003

Changed a file from non-ASCII to ASCII

ENTERED Changed the margins in cases where the sequence text was "wrapped" down to the next line. Edited a format error in the Current Application Data section, specifically: Edited the Current Application Data section with the actual current number. The number inputted by the applicant was the prior application data; or other _____. Added the mandatory heading and subheadings for "Current Application Data". Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer. Changed the spelling of a mandatory field (the headings or subheadings), specifically: Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place. Inserted colons after headings/subheadings. Headings edited included: Deleted extra, invalid, headings used by an applicant, specifically: Deleted: non-ASCII "garbage" at the beginning/end of files; secretary initials/filename at end of file; page numbers throughout text; other invalid text, such as _____. Inserted mandatory headings, specifically: Corrected an obvious error in the response, specifically: Edited identifiers where upper case is used but lower case is required, or vice versa. Corrected an error in the Number of Sequences field, specifically: A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted. Deleted ending stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____ Other:

Seq 64 - aligned amino acid nos.



RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/771,904A

DATE: 02/24/2003
TIME: 12:18:15

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02242003\I771904A.raw

4 <110> APPLICANT: DeBonte, Lorin R.
5 Fan, Zhegong
6 Miao, Guo-Hua
8 <120> TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
10 <130> FILE REFERENCE: 07148-063003
12 <140> CURRENT APPLICATION NUMBER: US 09/771,904A
13 <141> CURRENT FILING DATE: 2001-01-29
15 <150> PRIOR APPLICATION NUMBER: US 08/874,109
16 <151> PRIOR FILING DATE: 1997-06-12
18 <160> NUMBER OF SEQ ID NOS: 70
20 <170> SOFTWARE: FastSEQ for Windows Version 4.0
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1155
24 <212> TYPE: DNA
25 <213> ORGANISM: Brassica napus
27 <220> FEATURE:
28 <221> NAME/KEY: CDS
29 <222> LOCATION: (1)...(1152)
30 <223> OTHER INFORMATION: Wild type Fad2
32 <221> NAME/KEY: misc_feature
33 <222> LOCATION: 205
34 <223> OTHER INFORMATION: n = a, g, c, or t/u
W--> 36 <400> 1

37 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct	48
38 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser	
39 1 5 10 15	
41 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act	96
42 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	
43 20 25 30	
45 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg	144
46 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	
47 35 40 45	
49 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc	192
50 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser	
51 50 55 60	
W--> 53 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct	240
54 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro	
55 65 70 75 80	
57 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc	288
58 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	
59 85 90 95	
61 cta acc ggc gtc tgg gtc ata gcc cac gaa tgc ggc cac cac gcc ttc	336
62 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe	

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63	100	105	110	
65	agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc			384
66	Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser			
67	115	120	125	
69	ttc ctc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac			432
70	Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His			
71	130	135	140	
73	cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag			480
74	His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys			
75	145	150	155	160
77	aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg			528
78	Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu			
79	165	170	175	
81	gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg ccg ttg			576
82	Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu			
83	180	185	190	
85	tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt			624
86	Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg			
87	195	200	205	
89	tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc			672
90	Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu			
91	210	215	220	
93	cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc			720
94	Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu			
95	225	230	235	240
97	ttc cgt tac gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac			768
98	Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr			
99	245	250	255	
101	gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac			816
102	Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr			
103	260	265	270	
105	ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg			864
106	Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp			
107	275	280	285	
110	gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc			912
111	Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile			
112	290	295	300	
114	ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat			960
115	Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His			
116	305	310	315	320
118	ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg			1008
119	Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala			
120	325	330	335	
122	ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg			1056
123	Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val			
124	340	345	350	
126	gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg			1104
127	Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro			
128	355	360	365	

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130 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta 1152
 131 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 132 370 375 380
 134 tga 1155
 136 <210> SEQ ID NO: 2
 137 <211> LENGTH: 384
 138 <212> TYPE: PRT
 139 <213> ORGANISM: Brassica napus
 141 <220> FEATURE:
 142 <223> OTHER INFORMATION: Xaa = Phe, Leu, Ile, or Val
 144 <400> SEQUENCE: 2
 145 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 146 1 5 10 15
 147 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 148 20 25 30
 149 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 150 35 40 45
 151 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 152 50 55 60
 W--> 153 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 154 65 70 75 80
 155 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 156 85 90 95
 157 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 158 100 105 110
 159 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 160 115 120 125
 161 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 162 130 135 140
 164 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 165 145 150 155 160
 166 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 167 165 170 175
 168 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
 169 180 185 190
 170 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
 171 195 200 205
 172 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
 173 210 215 220
 174 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 175 225 230 235 240
 176 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
 177 245 250 255
 178 Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
 179 260 265 270
 180 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
 181 275 280 285
 182 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
 183 290 295 300

RAW SEQUENCE LISTING DATE: 02/24/2003
 PATENT APPLICATION: US/09/771,904A TIME: 12:18:15

Input Set : A:\PTO.AMC.txt
 Output Set: N:\CRF4\02242003\I771904A.raw

184 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 185 305 310 315 320
 186 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
 187 325 330 335
 188 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
 189 340 345 350
 190 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
 191 355 360 365
 192 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 193 370 375 380
 195 <210> SEQ ID NO: 3
 196 <211> LENGTH: 1155
 197 <212> TYPE: DNA
 198 <213> ORGANISM: Brassica napus
 200 <220> FEATURE:
 201 <221> NAME/KEY: CDS
 202 <222> LOCATION: (1)...(1152)
 203 <223> OTHER INFORMATION: G to A transversion mutation at nucleotide 316
 205 <221> NAME/KEY: misc_feature
 206 <222> LOCATION: 205
 207 <223> OTHER INFORMATION: n = a, g, c, or t/u
 W--> 209 <400> 3
 210 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct 48
 211 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 212 1 5 10 15
 214 gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96
 215 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 216 20 25 30
 218 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144
 219 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 220 35 40 45
 222 atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192
 223 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
 224 50 55 60
 W--> 226 tgc ttc tac tac ntc gcc acc act tac ttc cct ctc ctc cct cac cct 240
 227 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
 228 65 70 75 80
 230 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc caa ggg tgc gtc 288
 231 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 232 85 90 95
 234 cta acc ggc gtc tgg gtc ata gcc cac aag tgc ggc cac cac gcc ttc 336
 235 Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
 236 100 105 110
 238 agc gac tac cag tgg ctt gac gac acc gtc ggt ctc atc ttc cac tcc 384
 239 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 240 115 120 125
 242 ttc ctc gtc cct tac ttc tcc tgg aag tac agt cat cgc agc cac 432
 243 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
 244 130 135 140

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Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02242003\I771904A.raw

246 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag	480
247 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys	
248 145 150 155 160	
250 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg	528
251 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu	
252 165 170 175	
254 gga cgc acc gtg atg tta acg gtt cag ttc act ctc ggc tgg cgc ttg	576
255 Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu	
256 180 185 190	
258 tac tta gcc ttc aac gtc tcg gga aga cct tac gac ggc ggc ttc cgt	624
259 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg	
260 195 200 205	
262 tgc cat ttc cac ccc aac gct ccc atc tac aac gac cgc gag cgt ctc	672
263 Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu	
264 210 215 220	
266 cag ata tac atc tcc gac gct ggc atc ctc gcc gtc tgc tac ggt ctc	720
267 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu	
268 225 230 235 240	
272 ttc cgt tac gcc ggc cag gga gtg gcc tcg atg gtc tgc ttc tac	768
273 Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr	
274 245 250 255	
276 gga gtc ccg ctt ctg att gtc aat ggt ttc ctc gtg ttg atc act tac	816
277 Gly Val Pro Leu Leu Val Asn Gly Phe Leu Val Leu Ile Thr Tyr	
278 260 265 270	
280 ttg cag cac acg cat cct tcc ctg cct cac tac gat tcg tcc gag tgg	864
281 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp	
282 275 280 285	
284 gat tgg ttc agg gga gct ttg gct acc gtt gac aga gac tac gga atc	912
285 Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile	
286 290 295 300	
288 ttg aac aag gtc ttc cac aat att acc gac acg cac gtg gcc cat cat	960
289 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His	
290 305 310 315 320	
292 ccg ttc tcc acg atg ccg cat tat cac gcg atg gaa gct acc aag gcg	1008
293 Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala	
294 325 330 335	
296 ata aag ccg ata ctg gga gag tat tat cag ttc gat ggg acg ccg gtg	1056
297 Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val	
298 340 345 350	
300 gtt aag gcg atg tgg agg gag gcg aag gag tgt atc tat gtg gaa ccg	1104
301 Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro	
302 355 360 365	
304 gac agg caa ggt gag aag aaa ggt gtg ttc tgg tac aac aat aag tta	1152
305 Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu	
306 370 375 380	
308 tga	1155
310 <210> SEQ ID NO: 4	
311 <211> LENGTH: 384	
312 <212> TYPE: PRT	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 02/24/2003
PATENT APPLICATION: US/09/771,904A TIME: 12:18:16

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\02242003\I771904A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 205
Seq#:1; Xaa Pos. 69
Seq#:2; Xaa Pos. 69
Seq#:3; N Pos. 205
Seq#:3; Xaa Pos. 69
Seq#:4; Xaa Pos. 69